

us-10-687-361-1.rpr

Fri Sep 16 16:20:40 2005

GenCore version 5.1.6  
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OK nucleic - protein search, using frame\_plus\_n2p model

Run on: September 14, 2005, 17:46:10; Search time 46.5 Seconds  
(without alignments)  
4196.292 Million cell updates/sec

Title: US-10-687-361-1  
Perfect score: 1884  
Sequence: 1 tgcgtggccagcactcgagg.....ctaaaaa.....1014

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p model -DEV=xlp  
-Q/cgn2\_1/USFPO\_spool\_p/US10687361/runat 14092005 181747 29690/app\_query.fasta\_1.1159  
-DB=PIR -QFWT=fastan -SUPFLX=pr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THE SCORES=pcpt -THE MAX=100 -THE MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=pcpt -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10687361 @CNC1.1.63 @runat 14092005 181747 29690 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	852	45.2	163	2 S68520	Pin1 protein - hum
2	814	43.2	165	2 UC7136	peptidylprolyl iso
3	456.5	24.2	166	2 T08426	Pin1 protein homol
4	388.5	20.6	175	2 T41093	peptidyl-prolyl ci
5	356.5	18.9	170	2 S52764	B881 protein - yea
6	301	16.0	119	2 B84559	probable peptidyl-
7	180.5	9.6	292	2 S15269	post-translocation
8	177	9.4	247	2 A5934	peptidyl-prolyl ci
9	160	8.5	655	2 S82712	peptidyl-prolyl ci
10	158	8.4	142	2 E86392	hypothetical prote
11	157.5	8.4	126	2 T31601	hypothetical prote
12	155	8.2	660	1 QDBE3	BHLR1 protein - hu
13	154.5	8.2	775	1 QDBE11	immediate-early pr
14	153.5	8.1	331	2 AF3267	peptidyl-prolyl ci

15	149	7.9	273	2 S52412	major antigenic pe
16	148.5	7.9	333	2 A83797	protein secretion
17	148	7.9	469	1 S29126	properdin precurs
18	148	7.9	1596	2 A33106	neurogenic locus m
19	146.5	7.8	381	2 S16506	hypothetical prote
20	145.5	7.7	1496	1 CGH02V	collagen alpha 2(I
21	145	7.7	347	2 A81794	probable rotamase
22	145	7.7	348	2 B81216	peptidyl-prolyl ci
23	145	7.7	891	2 G84693	probable proline-r
24	145	7.7	820	2 T46412	ubiquitin-protein
25	142	7.5	615	2 A05269	collagen alpha 1(I
26	141	7.5	1497	2 T49607	collagen alpha 2(I
27	140.5	7.5	964	1 CGCH2S	hypothetical prote
28	140.5	7.5	1357	2 T29265	hypothetical prote
29	140	7.4	312	2 A61183	hypothetical prote
30	140	7.5	319	2 P75420	hypothetical prote
31	140	7.4	621	2 A83421	peptidyl-prolyl ci
32	139	7.4	264	2 D34768	ORF4 protein - Orf
33	138.5	7.4	418	2 T51442	hypothetical prote
34	138.5	7.4	552	2 P75311	ABC transporter, A
35	138.5	7.4	1106	2 JQ0405	hypothetical 119.5
36	138	7.3	93	2 B91217	peptidylprolyl iso
37	138	7.3	93	2 F86063	peptidylprolyl iso
38	138	7.3	93	2 S48658	peptidylprolyl iso
39	138	7.4	204	2 JQ0321	hypothetical 19.8K
40	138	7.3	325	2 T32248	hypothetical prote
41	137.5	7.3	528	2 B75310	conserved hypotet
42	137.5	7.3	862	2 T48289	hypothetical prote
43	137	7.3	93	2 AB0923	peptidyl-prolyl ci
44	136.5	7.2	1446	1 A45344	immediate-early pr
45	136	7.2	1414	1 S23809	collagen alpha 2(I

## ALIGNMENTS

## RESULT 1

S68520

Pin1 protein - human

C:Species: Homo sapiens (man)

C:Date: 15-Nov-1996 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C:Accession: S68520

R:Lin, K.P.; Hanes, S.D.; Hunter, T.

Nature 360, 544-547, 1996

A:Title: A human peptidyl-prolyl isomerase essential for regulation of mitosis.

A:Reference number: S68520; MUID:96195064; PMID:8606777

A:Accession: S68520

A&gt;Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-163 &lt;LINK&gt;

A:Cross-references: UNIPROT:Q13526; EMBL:U49070; NID:91332709; PIDN:AAC50492.1; PID:

C:Genetics:

A:Gene: GDB:PIN1; dod

A:Cross-references: GDB:5218381

C:Superfamily: Yeast B881 protein; WW repeat homology

F:5-43/Domain: WW repeat homology &lt;WWW1&gt;

Alignment Scores: 1.15e-53 Length: 163  
 Pred. No.: 852.00 Matches: 163  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 45.22% Gaps: 0

US-10-687-361-1 (1-1014) x S68520 (1-163)

Qy	25	ATGCGCGACGAGGAGAGCTCCCGCGCTGGGAGAGCCATGAGCGGAGCTCAGC 84
Db	1	MetAlaLeuGluGluLeuLeuProGlyTrpGluYsaArgMetSerArgSerGly 20
Qy	85	CGAGTGTAATCTTCAACACATCACTAACCCAGCCAGTGGAGCGGCCGAGCGAAC 144
Db	21	ArgValTyrTyrPheAsnHisIleThrAsnAlaSerGlnTrpLysProSerGlyAsn 40

